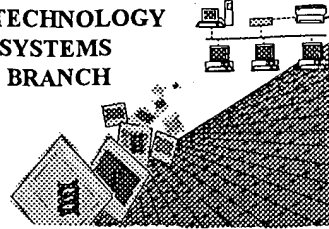


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/019,151

Source: 05/10

Date Processed by STIC: 3/19/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 101019,151

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|--|--|
| 1 | _____ Wrapped Nucleics
Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | ✓ _____ Misaligned Amino
Numbering | The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | _____ Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | _____ PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | _____ Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | _____ Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | _____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents. |
| 10 | _____ Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence. |
| 11 | _____ Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | _____ PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | _____ Misuse of n | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide. |



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,151

DATE: 03/19/2003

TIME: 14:33:58

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

4 <110> APPLICANT: Sagami Chemical Research Center, Protegene Inc.
 6 <120> TITLE OF INVENTION: Human proteins having hydrophobic domains and DNAs encoding
 7 these proteins
 9 <130> FILE REFERENCE: 661924
 11 <140> CURRENT APPLICATION NUMBER: US/10/019,151
 11 <141> CURRENT FILING DATE: 2003-01-31
 11 <150> PRIOR APPLICATION NUMBER: JP 11-178065
 12 <151> PRIOR FILING DATE: 1999-06-24
 14 <160> NUMBER OF SEQ ID NOS: 24

OK

pp 1-11
more throughout
Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 238
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Homo sapiens
 21 <400> SEQUENCE: 1
 22 Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val Asp Met
 23 1 5 10 15
 24 Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly
 25 20 25 30
 26 Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr
 E--> 27 35 35 40 45
 28 Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val
 E--> 29 50 55 60
 30 Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu
 E--> 31 65 70 75 80
 32 Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly
 E--> 33 85 90 95
 34 Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile
 E--> 35 100 105 110
 36 Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe
 E--> 37 115 120 125
 38 Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His
 E--> 39 130 135 140
 40 Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu
 E--> 41 145 150 155 160
 42 Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val
 E--> 43 165 170 175
 44 Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile
 E--> 45 180 185 190
 46 Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala

misaligned
amino acid
numbers
(see item 3
on Eva summary
sheet)

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/10/019,151

TIME: 14:33:58

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

```

E--> 47          195          200          205
48   Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly
E--> 49          210          215          220
50   Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser
E--> 51          225          230          235
53 <210> SEQ ID NO: 2
54 <211> LENGTH: 339
55 <212> TYPE: PRT
56 <213> ORGANISM: Homo sapiens
58 <400> SEQUENCE: 2
59   Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu
60     1          5          10          15
61   Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn
62          20          25          30
63   Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
64          35          40          45
65   Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
66          50          55          60
67   Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
68          65          70          75          80
69   Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
70          85          90          95
71   Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
72          100          105          110
73   Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
74          115          120          125
75   Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
76          130          135          140
77   Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
78          145          150          155          160
79   Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
80          165          170          175
81   Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
E--> 82          180 180          185          190
83   Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
E--> 84          195          200          205
85   Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
E--> 86          210          215          220
87   Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
E--> 88          225          230          235          240
89   Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
E--> 90          245          250          255
91   Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
E--> 92          260          265          270
93   Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
E--> 94          275          280          285
95   Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
E--> 96          290          295          300
97   Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys

```

*misaligned,
numbering*

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/10/019,151

TIME: 14:33:58

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

E--> 98 305 310 315 320
 99 Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
 E--> 100 325 330 336

101 Arg Arg Arg
 103 <210> SEQ ID NO: 3
 104 <211> LENGTH: 326
 105 <212> TYPE: PRT
 106 <213> ORGANISM: Homo sapiens
 108 <400> SEQUENCE: 3

109 Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr Leu
 110 1 5 10 15
 111 Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr Thr Ser
 112 20 25 30
 113 Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val Pro Lys Pro
 114 35 40 45
 115 Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser
 116 50 55 60
 117 Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn
 118 65 70 75 80
 119 Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe Arg Ser Gly
 120 85 90 95
 121 Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly Glu Arg Cys
 122 100 105 110
 123 Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu Ile Leu Trp
 124 115 120 125
 125 Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln Phe Ile Ser
 126 130 135 140
 127 Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys
 128 145 150 155 160
 129 Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val Leu Ser Gly
 130 165 170 175
 131 Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val Phe Gln Ala
 132 180 185 190
 133 Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val Trp Asn Tyr
 134 195 200 205
 135 Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala
 136 210 215 220
 137 Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe
 138 225 230 235 240
 139 Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn Cys Leu Pro
 140 245 250 255
 141 His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala Ala Pro Thr
 142 260 265 270
 143 Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln Pro Ile His
 144 275 280 285
 145 Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg Asn Lys Gly
 146 290 295 300
 E--> 147 Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val Arg Ser Ser
 148 305 310 315 320

*misaligned**invalid
amino acid
designator*

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/10/019,151

TIME: 14:33:58

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

```

149 Val Glu Glu Glu Gln Cys
150                               325
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 153
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 5
206 Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
207 1 5 10 15
208 Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
209 20 25 30
210 Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
211 35 40 45
212 Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
213 50 55 60
E--> 214 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gin Gly Lys Ala
215 65 70 75 80
E--> 216 Arg Leu Leu Thr His Trp Glu Gin Met Asp Tyr Gly Val Gin Phe Thr
217 85 90 95
218 Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu
219 100 105 110
E--> 220 Thr Ser Phe Tyr Thr Lys Tyr Asp Gin Ile His Phe Val Leu Asn Thr
221 115 120 125
E--> 222 Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gin Leu His Gly
223 130 135 140
224 Val Arg Ile Phe Gly Ile Asn Lys Tyr
225 145 150
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 200
256 <212> TYPE: PRT
257 <213> ORGANISM: Homo sapiens
259 <400> SEQUENCE: 7
E--> 260 Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala
261 1 5 10 15
262 Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp
263 20 25 30
264 Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe
265 35 40 45
266 Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg
267 50 55 60
268 Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu
269 65 70 75 80
270 Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val
271 85 90 95
272 Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe
273 100 105 110
274 Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser
275 115 120 125
276 Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val

```

*Invalid**use lower-case "l"
not numeral
"1"*

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/10/019,151

TIME: 14:33:58

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

277 130 135 140
 278 Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys
 279 145 150 155 160
 280 Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met
 281 165 170 175
 282 Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr
 283 180 185 190
 284 Leu Glu Lys Thr Ile His Glu Glu
 285 195 200
 631 <210> SEQ ID NO: 19
 632 <211> LENGTH: 1125
 633 <212> TYPE: DNA
 634 <213> ORGANISM: Homo sapiens
 636 <220> FEATURE:
 637 <221> NAME/KEY: CDS
 638 <222> LOCATION: (71)...(1051)
 640 <400> SEQUENCE: 19

see p. 6

641 ttaaaccacaaa gggacttgga gtgcagatgg catccttcgg ttcttccaga caagctgcaa 60
 642 gacgctgacc atg gcc aag atg gag ctc tcg aag gcc ttc tct ggc cag 109
 643 Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln
 644 1 5 10
 645 cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157
 646 Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser
 647 15 20 25
 648 aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205
 650 Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val
 651 30 35 40 45
 652 ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg 253
 653 Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met
 654 50 55 60
 655 cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag gtg gta 301
 656 Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val
 657 65 70 75
 658 caa tac aac tgg gag act ggg gat gac cgg ttc tcc ttc cgg agc ttc 349
 659 Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe
 660 80 85 90
 661 cgg agt ggc atg tgg cta tcc tgt gag gaa act gtg gaa gaa cca ggg 397
 662 Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly
 663 95 100 105
 664 gag agg tgc cga agt ttc att gaa ctt aca cca gcc aag aga gaa 445
 665 Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu
 666 110 115 120 125
 667 atc cta tgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa 493
 W--> 668 Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln
 669 130 135 140
 670 ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac 541
 671 Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn
 672 145 150 155
 673 cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct gtt tcc tct gtc 589

Gly

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/10/019,151

TIME: 14:33:58

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

674 Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val
 675 160 165 170
 676 ctg tca ggg ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc 637
 W--> 677 Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val
 678 175 180 185
 679 ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt 685
 680 Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val
 681 190 195 200 205
 682 tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc 733
 683 Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys
 684 210 215 220
 685 tgc atg gcg tcg gct gtc acc acc ttc aac acg tac acc agg atg gtg 781
 686 Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val
 687 225 230 235
 688 ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac 829
 689 Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn
 690 240 245 250
 691 tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca 877
 692 Cys Leu Pro His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala
 693 255 260 265
 694 gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag 925
 695 Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln
 696 270 275 280 285
 697 ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg 973
 698 Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg
 699 290 295 300
 E--> 700 aac aag gga ttt caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt 1021
 701 Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val
 702 305 310 315
 703 agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggtttgg gg 1070
 704 Arg Ser Ser Val Glu Glu Glu Gln Cys
 705 320 325
 706 agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc 1125
 708 <210> SEQ ID NO: 20
 709 <211> LENGTH: 1734
 710 <212> TYPE: DNA
 711 <213> ORGANISM: Homo sapiens
 713 <220> FEATURE:
 714 <221> NAME/KEY: CDS
 715 <222> LOCATION: (40)...(1014)
 717 <400> SEQUENCE: 20
 718 ctcttgccgc gcccgtagcg gcccgcccg gcaggccgg atg gcg gcc gcg gct 54
 719 Met Ala Ala Ala Ala
 720 1 5
 721 ccg gag aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg 102
 722 Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu
 723 10 15 20
 724 gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa 150
 725 Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu

do not
 show "i"
 in the
 sequence.
 Use "n" and
 explain in
 <2207-223>
 section

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/10/019,151

TIME: 14:33:58

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

726 25 30 35
 727 gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg 198
 728 Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu
 729 40 45 50
 730 cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag 246
 731 Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu
 732 55 60 65
 E--> 733 **aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat det** 294 *Invalid*
 734 Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro
 735 70 75 80 85
 736 gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata 342
 737 Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile
 738 90 95 100
 739 tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca 390
 740 Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala
 741 105 110 115
 742 gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca 438
 743 Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala
 744 120 125 130
 745 atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat 486
 746 Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr
 747 135 140 145
 748 gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta 534
 749 Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val
 750 150 155 160 165
 751 tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg 582
 752 Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met
 753 170 175 180
 754 agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta 630
 755 Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu
 756 185 190 195
 757 aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg 678
 758 Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro
 759 200 205 210
 760 gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg 726
 761 Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp
 762 215 220 225
 763 ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc 774
 764 Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe
 765 230 235 240 245
 766 tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca 822
 767 Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala
 768 250 255 260
 769 gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac 870
 770 Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His
 771 265 270 275
 772 tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag 918
 773 Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln
 774 280 285 290

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/10/019,151

TIME: 14:33:58

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

```

775   aaa atc tct gtc aga act gtg aca atc ata aga ggc atc gtt ttt ttg      966
776   Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu
777       295              300              305
778   gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt      1011
779   Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe
780   310              315              320
781   taacgctgt ttgttcatct atatttagtt taaaataggt agtattatct ttctgtacat  1070
782   agtgtacatt acaactaaaa gtgatggaaa aatactgtat tttgtagcac tgattttgtg  1130
783   agtttgaccc attattatgt ctgagatata atcattgatt ctatttgtaa caaggagttt  1190
784   taaaagaaac ctgacttcta agtgtgggtt tttcttctct ccaacataat tatgttaata  1250
785   tggctctcat ttttcttttg gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt  1310
786   ctttcagcac tgaccctttt ttaaggaata caaattttct ctttcacac ttaggtgttt  1370
787   taagatgttt accttaaagt ttttcttggg gaaagaatga attaatttct atttcttaaa  1430
788   acatttcctt gagccagtaa acagtagttt aatcattggt cttttcaaaa ctagggtgttt  1490
789   aaaaaagag acatatatga tattgctgtt atatcaataa catggcacia caagaactgt  1550
790   ctgccaggtc attcttcctc tttttttttt aattgggtag gacaccaat ataaaaacag  1610
791   tcaatatttg acaatgtgga attaccaa ataaagagaa tactatgaat gtattcatat  1670
792   tttttctata ttgaataaac aatgtaacat agataacaat ataaataaaa gtggtatgac  1730
793   cagt      1734
794   <210> SEQ ID NO: 24
795   <211> LENGTH: 823
796   <212> TYPE: DNA
797   <213> ORGANISM: Homo sapiens
798   <220> FEATURE:
799   <221> NAME/KEY: CDS
800   <222> LOCATION: (58)...(627)
801   <400> SEQUENCE: 24
802   acacacacat ctgcacctca accacagact acacttgctg aactggctcc tgggggcc      57
803   atg agg ctg tca ctg cca ctg ctg ctg ctg ctg gga gcc tgg gcc      105
804   Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala
805       1              5              10              15
806   atc cca ggg ggc ctc ggg gac agg gcg cca ctc aca gcc aca gcc cca      153
807   Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
808       20              25              30
809   caa ctg gat gat gag gag atg tac tca gcc cac atg ccc gct cac ctg      201
810   Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
811       35              40              45
812   cgc tgt gat gcc tgc aga gct gtg gct tac cag atg tgg caa aat ctg      249
813   Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
814       50              55              60
815   gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg      297
816   Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
817       65              70              75              80
818   gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc      345
819   W--> 999 Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Ara Ser Cys Ser
820       85              90              95
821   cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt      393
822   Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
823       100              105              110

```

RAW SEQUENCE LISTING

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1004	ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg	441
1005	Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val	
1006	115 120 125	
1007	atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg	489
1008	Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu	
1009	130 135 140	
1010	cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa	537
1011	His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln	
1012	145 150 155 160	
1013	caa ggc cga ggg gct ctg gag gca ttg cta tgt ggg gga ccc cag ggg	585
1014	Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly	
W--> 1015	165 170 175 ← misaligned	
1016	gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc	630
1017	Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu	
W--> 1018	180 185	
1019	tggactctac cctcctctga aagaagctgg ggcttgctct gacgggtctcc actcccgtct	690
1020	gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccatacctgcc tccctcctcc	750
1021	agcctcaggg cactcggggc tgggtgggag tcaacgcctt cccctctgga ctcaaataaa	810
1022	acccagtgac ctc	823
E--> 1024	ny_maIn 322915v1 delete	

See following pages for more error

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<400> 17
 ctgacctctg ggaaggaaat acattataga gtgggaaatt tttatcattt tgaaccaaga 60
 ttcttctaaa gaaagaaaga ctgattaata aaatgtggca gctgtgctct tcaaggcatt 120
 tatagtgtat atagtttttag aaaaacagtc ccaccactta agcatagatg taatttacta 180
 ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228
 Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val
 1 5 10
 gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276
 Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe
 15 20 25 30
 act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324
 Thr Gly Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu
 35 35 40 45
 aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372
 Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu
 50 55 60

*misaligned
 number
 →*

*Please correct all misaligned amino
 numbers throughout sequence listing*

10/019,151 11

Sequence 18

tgt	ggc	ttg	gag	tat	aat	tta	gat	tat	aca	gaa	ctt	ggc	ctg	caa	aaa	549
Cys	Gly	Leu	Glu	Tyr	Asn	Leu	Asp	Tyr	Thr	Glu	Leu	Gly	Leu	Gln	Lys	
130					135					140					145	

invalid

Please ensure that all
amino acids are valid.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/019,151

DATE: 03/19/2003

TIME: 14:33:59

Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:27 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
 M:332 Repeated in SeqNo=1
 L:82 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
 M:332 Repeated in SeqNo=2
 L:147 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
 L:214 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
 L:216 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:2
 L:220 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
 L:222 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
 L:260 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
 L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:512 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:515 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:521 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:527 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
 L:574 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:576 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:577 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:579 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:583 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:586 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:588 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:589 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:592 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:594 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:595 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:598 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:601 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:604 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:607 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:610 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:613 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:617 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
 L:668 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:677 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:700 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:733 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/019,151

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Input Set : A:\(01997.025700) Sequence Listing.txt

Output Set: N:\CRF4\03192003\J019151.raw

L:825 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:999 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1015 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1018 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:1024 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:24
L:1024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:823
L:1024 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:831 SEQ:24
L:1024 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:1024 M:112 C: (48) String data converted to lower case,
L:1024 M:252 E: No. of Seq. differs, <211> LENGTH:Input:823 Found:831 SEQ:24